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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schlessinger, Joseph
Sap, Jan M.
- (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
PHOSPHATASE-ALPHA
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 AVENUE OF THE AMERICAS
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/015,985
 - (B) FILING DATE: 10-FEB-1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-020
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741/8864
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
1 5 10 15
Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
20 25 30
Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
35 40 45
Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
50 55 60

Phe S r Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
 65 70 75 80
 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
 85 90 95
 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
 100 105 110
 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 115 120 125
 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
 130 135 140
 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
 145 150 155 160
 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
 165 170 175
 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
 180 185 190
 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
 195 200 205
 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
 210 215 220
 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
 225 230 235 240
 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
 245 250 255
 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
 260 265 270
 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
 275 280 285
 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
 290 295 300
 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
 305 310 315 320
 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
 325 330 335
 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
 340 345 350
 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
 355 360 365
 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
 370 375 380
 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile
 385 390 395 400
 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr
 405 410 415
 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro

| 420 | | | | | 425 | | | | | 430 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Tyr | Ala | Gly | Ala | Ile | Val | Val | His | Cys | Ser | Ala | Gly | Val | Gly | Arg |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Thr | Gly | Thr | Phe | Val | Val | Ile | Asp | Ala | Met | Leu | Asp | Met | Met | His | Thr |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Glu | Arg | Lys | Val | Asp | Val | Tyr | Gly | Phe | Val | Ser | Arg | Ile | Arg | Ala | Gln |
| 465 | | | | | 470 | | | | | 475 | | | | 480 | |
| Arg | Cys | Gln | Met | Val | Gln | Thr | Asp | Met | Gln | Tyr | Val | Phe | Ile | Tyr | Gln |
| | | | 485 | | | | | | 490 | | | | | 495 | |
| Ala | Leu | Leu | Glu | His | Tyr | Leu | Tyr | Gly | Asp | Thr | Glu | Leu | Glu | Val | Thr |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Ser | Leu | Glu | Thr | His | Leu | Gln | Lys | Ile | Tyr | Asn | Lys | Ile | Pro | Gly | Thr |
| | 515 | | | | | | 520 | | | | | 525 | | | |
| Ser | Asn | Asn | Gly | Leu | Glu | Glu | Glu | Phe | Lys | Lys | Leu | Thr | Ser | Ile | Lys |
| | 530 | | | | | | 535 | | | | 540 | | | | |
| Ile | Gln | Asn | Asp | Lys | Met | Arg | Thr | Gly | Asn | Leu | Pro | Ala | Asn | Met | Lys |
| 545 | | | | | 550 | | | | | 555 | | | | 560 | |
| Lys | Asn | Arg | Val | Leu | Gln | Ile | Ile | Pro | Tyr | Glu | Phe | Asn | Arg | Val | Ile |
| | | | 565 | | | | | | 570 | | | | | 575 | |
| Ile | Pro | Val | Lys | Arg | Gly | Glu | Glu | Asn | Thr | Asp | Tyr | Val | Asn | Ala | Ser |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Phe | Ile | Asp | Gly | Tyr | Arg | Gln | Lys | Asp | Ser | Tyr | Ile | Ala | Ser | Gln | Gly |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Pro | Leu | Leu | His | Thr | Ile | Glu | Asp | Phe | Trp | Arg | Met | Ile | Trp | Glu | Trp |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Lys | Ser | Cys | Ser | Ile | Val | Met | Leu | Thr | Glu | Leu | Glu | Glu | Arg | Gly | Gln |
| 625 | | | | | 630 | | | | | 635 | | | | 640 | |
| Glu | Lys | Cys | Ala | Gln | Tyr | Trp | Pro | Ser | Asp | Gly | Leu | Val | Ser | Tyr | Gly |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Asp | Ile | Thr | Val | Glu | Leu | Lys | Lys | Glu | Glu | Glu | Cys | Glu | Ser | Tyr | Thr |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Val | Arg | Asp | Leu | Leu | Val | Thr | Asn | Thr | Arg | Glu | Asn | Lys | Ser | Arg | Gln |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Ile | Arg | Gln | Phe | His | Phe | His | Gly | Trp | Pro | Glu | Val | Gly | Ile | Pro | Ser |
| | 690 | | | | | 695 | | | | | 700 | | | | |
| Asp | Gly | Lys | Gly | Met | Ile | Ser | Ile | Ile | Ala | Ala | Val | Gln | Lys | Gln | Gln |
| 705 | | | | | 710 | | | | 715 | | | | | 720 | |
| Gln | Gln | Ser | Gly | Asn | His | Pro | Ile | Thr | Val | His | Cys | Ser | Ala | Gly | Ala |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Gly | Arg | Thr | Gly | Thr | Phe | Cys | Ala | Leu | Ser | Thr | Val | Leu | Glu | Arg | Val |
| | | | 740 | | | | | 745 | | | | | 750 | | |
| Lys | Ala | Glu | Gly | Ile | Leu | Asp | Val | Phe | Gln | Thr | Val | Lys | Ser | Leu | Arg |
| | 755 | | | | | 760 | | | | | | 765 | | | |
| Leu | Gln | Arg | Pro | His | Met | Val | Gln | Thr | Leu | Glu | Gln | Tyr | Glu | Phe | Cys |
| | 770 | | | | | 775 | | | | | | 780 | | | |

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|--|------|
| ATGGATTCTT GGTTCATTCT TGTTCTGCTC GGCAGTGGTC TGATATGTGT CAGTGCCAAC | 60 |
| AATGCTACCA CAGTTGCACC TTCTGTAGGA ATTACAAGAT TAATTAAGTC ATCAACGGCA | 120 |
| GAACCAAGTA AAGAAGAGGC CAAAAGTTCA AATCCAAGTT CTTCAGTAACT TTCTCTTTCT | 180 |
| GTGGCACCAC CATTGAGCCC AAATATAACT CTGGGACCCA CCTATTTAAC CACTGTCAAT | 240 |
| TCTTCAGACT CTGACAATGG GACCACAAGA ACAGCAAGCA CCAATTCTAT AGGCATTACA | 300 |
| ATTTACACCA ATGGAACGTG GCTTCCAGAT AACCAGTTCA CGGATGCCAG AACAGAACCC | 360 |
| TGGGAGGGGA ATTCCAGCAC CGCAGCAACC ACTCCAGAAA CTTTCCCTCC TTCAGGTAAT | 420 |
| TCTGACTCGA AGGACAGAAG AGATGAGACA CCAATTATTG CGGTGATGGT GGCCCTGTCC | 480 |
| TCTCTGCTAG TGATCGTGTT TATTATCATA GTTTTGTACA TGTTAAGGTT TAAGAAATAC | 540 |
| AAGCAAGCTG GGAGCCATTC CAATTCTTTC CGCTTATCCA ACGGCCGCAC TGAGGATGTG | 600 |
| GAGCCCCAGA GTGTGCCACT TCTGGCCAGA TCCCCAAGCA CCAACAGGAA ATACCCACCC | 660 |
| CTGCCCCTGG ACAAGCTGGA AGAGGAAATT AACCGGAGAA TGGCAGACGA CAATAAGCTC | 720 |
| TTCAGGGAGG AATTCAACGC TCTCCCTGCA TGTCTATACC AGGCCACCTG TGAGGCTGCT | 780 |
| TCCAAGGAGG AAAACAAGGA AAAAAATCGA TATGTAAACA TCTTGCCCTA TGACCACTCT | 840 |
| AGAGTCCACC TGACACCGGT TGAAGGGGTT CCAGATTCTG ATTACATCAA TGCTTCATTC | 900 |
| ATCAACGGTT ACCAAGAAAA GAACAAATTC ATTGCTGCAC AAGGACCAAA AGAAGAAACG | 960 |
| GTGAATGATT TCTGGCGGAT GATCTGGGAA CAAAACACAG CCACCATCGT CATGGTTACC | 1020 |
| AACCTGAAGG AGAGAAAGGA GTGCAAGTGC GCCCAGTACT GGCCAGACCA AGGCTGCTGG | 1080 |
| ACCTATGGGA ATATTCGGGT GTCTGTAGAG GATGTGACTG TCCTGGTGGA CTACACAGTA | 1140 |
| CGGAAGTTCT GCATCCAGCA GGTGGGCGAC ATGACCAACA GAAAGCCACA GCGCCTCATC | 1200 |
| ACTCAGTTCC ACTTTACCAG CTGGCCAGAC TTTGGGGTGC CTTTACCCC GATCGGCATG | 1260 |
| CTCAAGTTCC TCAAGAAGGT GAAGGCCTGT AACCTCAGT ATGCAGGGGC CATCGTGGTC | 1320 |
| CACTGCAGTG CAGGTGTAGG GCGTACAGGT ACCTTTGTCT TCATTGATGC CATGCTGGAC | 1380 |
| ATGATGCATA CAGAACGGAA GGTGGACGTG TATGGCTTTG TGAGCCGGAT CCGGGCACAG | 1440 |
| CGCTGCCAGA TGGTGCAAAC CGATATGCAG TATGTCTTCA TATACCAAGC CCTTCTGGAG | 1500 |

| | |
|---|------|
| CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA | 1560 |
| ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA | 1620 |
| ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG | 1680 |
| AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG | 1740 |
| CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG | 1800 |
| GACTCCTATA TCGCCAGOCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG | 1860 |
| ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG | 1920 |
| GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG | 1980 |
| GAAGTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC | 2040 |
| ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG | 2100 |
| GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG | 2160 |
| CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG | 2220 |
| ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC | 2280 |
| TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG | 2340 |
| TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC | 2400 |
| TTCAAGTAA | 2409 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Trp | Phe | Ile | Leu | Val | Leu | Phe | Gly | Ser | Gly | Leu | Ile | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ser | Ala | Asn | Asn | Ala | Thr | Thr | Val | Ser | Pro | Ser | Leu | Gly | Thr | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Leu | Ile | Lys | Thr | Ser | Thr | Thr | Glu | Leu | Ala | Lys | Glu | Glu | Asn | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Ser | Asn | Ser | Thr | Ser | Ser | Val | Ile | Ser | Leu | Ser | Val | Ala | Pro | Thr |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Phe | Ser | Pro | Asn | Leu | Thr | Leu | Glu | Pro | Thr | Tyr | Val | Thr | Thr | Val | Asn |
| | | 65 | | | 70 | | | | 75 | | | | | | 80 |
| Ser | Ser | His | Ser | Asp | Asn | Gly | Thr | Arg | Arg | Ala | Ala | Ser | Thr | Glu | Ser |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Gly | Gly | Thr | Thr | Ile | Ser | Pro | Asn | Gly | Ser | Trp | Leu | Ile | Glu | Asn | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Thr | Asp | Ala | Ile | Thr | Glu | Pro | Trp | Glu | Gly | Asn | Ser | Ser | Thr | Ala |
| | | | 115 | | | | 120 | | | | | | 125 | | |

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

[illegible]

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|--|------|
| GAATTCCGGC GAGTGAGGCG CTGACAGGGA CTCGCGGGGG CATCTTGCAC AGACCCCTGG | 60 |
| ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCGGCTTCTC CTCGCCATGG | 120 |
| AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT | 180 |
| GGGCCGAGAG CCCGGTCCTG AGGCGGAGCT GCCGTGCGCG TCCCCCGCGG TCCCGCCCCA | 240 |
| GCGCCGGGCT CGGTCAGCAT GGATTCTGG TTCATTCTTG TCCTGTTTGG CAGTGGTCTA | 300 |
| ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA | 360 |
| ATTAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAAA TTCAACCTCT | 420 |
| TCAGTAATTT CTCTTTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCACC | 480 |
| TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGC | 540 |
| GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCACG | 600 |
| GATGCCATAA CAGAACCCTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC | 660 |
| TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA | 720 |
| GTAATCGTGT TTATTATCAT AGTTCTGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT | 780 |
| GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCCAA | 840 |
| AGTGTACCAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG | 900 |
| GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA | 960 |
| GAATTCAACG CTCTCCCTGC TTGTCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA | 1020 |
| GAAAACAAGG AAAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC | 1080 |
| CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC | 1140 |
| TACCAGGAAA AGAACAAATT CATCGCTGCA CAAGGACCAA AAGAAGAAAC AGTGAATGAC | 1200 |
| TTCTGGAGAA TGATATGGGA ACAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG | 1260 |
| GAGAGAAAGG AGTGTAATG TGCCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG | 1320 |
| AATGTCCGTG TGTCTGTCTG GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC | 1380 |
| TCGATCCAGC AGGTGGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC | 1440 |
| CACTTCACCA GCTGGCCAGA CTTTGGGGTG CTTTTCACCC CAATTGGCAT GCTCAAGTTC | 1500 |
| CTCAAGAAGG TGAAGGCCTG TAACCCTCAG TACGCAGGGG CTATCGTGGT CCACTGCAGT | 1560 |
| GCAGGTGTAG GGCGCACTGG CACCTTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT | 1620 |
| TCGGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCCA GCGCTGCCAG | 1680 |
| ATGGTACAGA CAGACATGCA GTACGTCTTC ATATACCAGG CCCTTCTGGA GCATTATCTG | 1740 |
| TATGGGGACA CAGAACTGGA AGTGACTTCT CTAGAAACCC ACCTACAAA AATTTATAAC | 1800 |
| AAGATCCCAG GGAAGTAGCA CAACGGGTTA GAGGAGGAGT TTAAGAAATT AACTTCAATC | 1860 |
| AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG | 1920 |

| | |
|---|------|
| GTTTTACAGA TCATTCCATA TGAATTTAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA | 1980 |
| GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC | 2040 |
| ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCGAAT GATCTGGGAG | 2100 |
| TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT | 2160 |
| GCCCAGTACT GGCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG | 2220 |
| AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG | 2280 |
| AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC | 2340 |
| AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG | 2400 |
| GGGAACCATC CCATCACTGT GCACTGCAGT GCCGGGGCAG GACGGACAGG AACCTTCTGT | 2460 |
| GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT | 2520 |
| GTCAAGAGCC TCGGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATTC | 2580 |
| TGCTACAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA | 2640 |
| CAGGTGACAA GGCCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTAATA TTCTGTTTTT | 2700 |
| GTTAATATAC CCAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC | 2760 |
| TATTACCTGT TAGATGGAGA TTTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTTCCA | 2820 |
| GTGTTTTATT GGGAAATTAA TAGTGTGATA TTTGGGTGA TATAATGAAT TC | 2872 |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Asn | Lys | Asn | Arg | Tyr | Val | Asp | Ile | Leu | Pro | Tyr | Asp | Tyr | Asn |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Arg | Val | Glu | Leu | Ser | Glu | Ile | Asn | Gly | Asp | Ala | Gly | Ser | Asn | Tyr | Ile |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Asn | Ala | Ser | Tyr | Ile | Asp | Gly | Phe | Lys | Glu | Pro | Arg | Lys | Tyr | Ile | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Gln | Gly | Pro | Arg | Asp | Glu | Thr | Val | Asp | Asp | Phe | Trp | Arg | Met | Ile |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Trp | Glu | Gln | Lys | Ala | Thr | Val | Ile | Val | Met | Val | Thr | Arg | Cys | Glu | Glu |
| 65 | | | 70 | | | | | | 75 | | | | | 80 | |
| Gly | Asn | Arg | Asn | Lys | Cys | Ala | Glu | Tyr | Trp | Pro | Ser | Met | Glu | Glu | Gly |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Thr | Arg | Ala | Phe | Gly | Asp | Val | Val | Val | Lys | Ile | Asn | Gln | His | Lys | Arg |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Cys | Pro | Asp | Tyr | Ile | Ile | Gln | Lys | Leu | Asn | Ile | Val | Asn | Lys | Lys | Glu |

| | | |
|---|-----|-----|
| 115 | 120 | 125 |
| Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro | | |
| 130 | 135 | 140 |
| Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu Arg Arg | | |
| 145 | 150 | 155 |
| Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His | | |
| | 165 | 170 |
| Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala | | |
| | 180 | 185 |
| Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr | | |
| | 195 | 200 |
| Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala | | |
| | 210 | 215 |
| Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu | | |
| 225 | 230 | 235 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|-----|
| Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser | |
| 1 | 15 |
| Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile | |
| 20 | 30 |
| Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala | |
| 35 | 45 |
| Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile | |
| 50 | 60 |
| Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu | |
| 65 | 80 |
| Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp | |
| 85 | 95 |
| Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val | |
| 100 | 110 |
| Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr | |
| 115 | 125 |
| Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp | |
| 130 | 140 |
| Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu | |
| 145 | 155 |
| Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val | |

| | | | | | |
|---|-----|--|-----|--|-----|
| | 165 | | 170 | | 175 |
| His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp | | | | | |
| | 180 | | 185 | | 190 |
| Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly | | | | | |
| | 195 | | 200 | | 205 |
| Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp | | | | | |
| | 210 | | 215 | | 220 |
| Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu | | | | | |
| | 225 | | 230 | | 235 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|-------------|
| Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser | |
| 1 | 5 10 15 |
| Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp | |
| | 20 25 30 |
| Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr | |
| | 35 40 45 |
| Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg | |
| | 50 55 60 |
| Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu | |
| 65 | 70 75 80 |
| Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly | |
| | 85 90 95 |
| Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val | |
| | 100 105 110 |
| Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile | |
| | 115 120 125 |
| Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln | |
| | 130 135 140 |
| Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu | |
| 145 | 150 155 160 |
| Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala | |
| | 165 170 175 |
| Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly | |
| | 180 185 190 |
| Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly | |
| | 195 200 205 |
| Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn | |

| | | |
|---|-----|---------|
| 210 | 215 | 220 |
| Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Thr Leu | | |
| 225 | 230 | 235 240 |
| Val Glu | | |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Asn | Lys | His | Lys | Asn | Arg | Tyr | Ile | Asn | Ile | Leu | Ala | Tyr | Asp | His | Ser | 1 | 5 | 10 | 15 |
| Arg | Val | Lys | Leu | Arg | Pro | Leu | Pro | Gly | Lys | Asp | Ser | Lys | His | Ser | Asp | 20 | 25 | 30 | |
| Tyr | Ile | Asn | Ala | Asn | Tyr | Val | Asp | Gly | Tyr | Asn | Lys | Ala | Lys | Ala | Tyr | 35 | 40 | 45 | |
| Ile | Ala | Thr | Gln | Gly | Pro | Leu | Lys | Ser | Thr | Phe | Glu | Asp | Phe | Trp | Arg | 50 | 55 | 60 | |
| Met | Ile | Trp | Glu | Gln | Asn | Thr | Gly | Ile | Ile | Val | Met | Ile | Thr | Asn | Leu | 65 | 70 | 75 | |
| Val | Glu | Lys | Gly | Arg | Arg | Lys | Cys | Asp | Gln | Tyr | Trp | Pro | Thr | Glu | Asn | 85 | 90 | 95 | |
| Ser | Glu | Glu | Tyr | Gly | Asn | Ile | Ile | Val | Thr | Leu | Lys | Ser | Thr | Lys | Ile | 100 | 105 | 110 | |
| His | Ala | Cys | Tyr | Thr | Val | Arg | Arg | Phe | Ser | Ile | Arg | Asn | Thr | Lys | Val | 115 | 120 | 125 | |
| Lys | Lys | Gly | Gln | Lys | Gly | Asn | Pro | Lys | Gly | Arg | Gln | Asn | Glu | Arg | Val | 130 | 135 | 140 | |
| Val | Ile | Gln | Tyr | His | Tyr | Thr | Gln | Trp | Pro | Asp | Met | Gly | Val | Pro | Glu | 145 | 150 | 155 | |
| Tyr | Ala | Leu | Pro | Val | Leu | Thr | Phe | Val | Arg | Arg | Ser | Ser | Ala | Ala | Arg | 165 | 170 | 175 | |
| Met | Pro | Glu | Thr | Gly | Pro | Val | Leu | Val | His | Cys | Ser | Ala | Gly | Val | Gly | 180 | 185 | 190 | |
| Arg | Thr | Gly | Thr | Tyr | Ile | Val | Ile | Asp | Ser | Met | Leu | Gln | Gln | Ile | Lys | 195 | 200 | 205 | |
| Asp | Lys | Ser | Thr | Val | Asn | Val | Leu | Gly | Phe | Leu | Lys | His | Ile | Arg | Thr | 210 | 215 | 220 | |
| Gln | Arg | Asn | Tyr | Leu | Val | Gln | Thr | Glu | Glu | Gln | Tyr | Ile | Phe | Ile | His | 225 | 230 | 235 | |
| Asp | Ala | Leu | Leu | Glu | 245 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser
1          5          10          15
Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp
20          25          30
Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr
35          40          45
Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg
50          55          60
Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu
65          70          75          80
Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly
85          90          95
Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val
100         105         110
Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr
115         120         125
Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa
130         135         140
Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly
145         150         155         160
Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa
165         170         175
Ala Ala Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala
180         185         190
Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln
195         200         205
Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His
210         215         220
Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa
225         230         235         240
Phe Ile His Xaa Ala Leu Xaa Glu
245

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Ser | Lys | Asn | Arg | Asn | Ser | Asn | Val | Ile | Pro | Tyr | Asp | Tyr | Asn | 1 | 5 | 10 | 15 |
| Arg | Val | Pro | Leu | Lys | His | Glu | Leu | Glu | Met | Ser | Lys | Glu | Ser | Glu | His | 20 | 25 | 30 | |
| Asp | Ser | Asp | Glu | Ser | Ser | Asp | Asp | Asp | Ser | Asp | Ser | Glu | Glu | Pro | Ser | 35 | 40 | 45 | |
| Lys | Tyr | Ile | Asn | Ala | Ser | Phe | Ile | Met | Ser | Tyr | Trp | Lys | Pro | Glu | Val | 50 | 55 | 60 | |
| Met | Ile | Ala | Ala | Gln | Gly | Pro | Leu | Lys | Glu | Thr | Ile | Gly | Asp | Phe | Trp | 65 | 70 | 75 | 80 |
| Gln | Met | Ile | Phe | Gln | Arg | Lys | Val | Lys | Val | Ile | Val | Met | Leu | Thr | Glu | 85 | 90 | 95 | |
| Leu | Lys | His | Gly | Asp | Gln | Glu | Ile | Cys | Ala | Gln | Tyr | Trp | Gly | Glu | Gly | 100 | 105 | 110 | |
| Lys | Gln | Thr | Tyr | Gly | Asp | Ile | Glu | Val | Asp | Leu | Lys | Asp | Thr | Asp | Lys | 115 | 120 | 125 | |
| Ser | Ser | Thr | Tyr | Thr | Leu | Arg | Val | Phe | Glu | Leu | Arg | His | Ser | Lys | Arg | 130 | 135 | 140 | |
| Lys | Asp | Ser | Arg | Thr | Val | Tyr | Gln | Tyr | Gln | Tyr | Thr | Asn | Trp | Ser | Val | 145 | 150 | 155 | 160 |
| Glu | Gln | Leu | Pro | Ala | Glu | Pro | Lys | Glu | Leu | Ile | Ser | Met | Ile | Gln | Val | 165 | 170 | 175 | |
| Val | Lys | Gln | Lys | Leu | Pro | Gln | Lys | Asn | Ser | Ser | Glu | Gly | Asn | Lys | His | 180 | 185 | 190 | |
| His | Lys | Ser | Thr | Pro | Leu | Leu | Ile | His | Cys | Arg | Asp | Gly | Ser | Gln | Gln | 195 | 200 | 205 | |
| Thr | Gly | Ile | Phe | Cys | Ala | Leu | Leu | Asn | Leu | Leu | Glu | Ser | Ala | Glu | Thr | 210 | 215 | 220 | |
| Glu | Glu | Val | Val | Asp | Ile | Phe | Gln | Val | Val | Lys | Ala | Leu | Arg | Lys | Ala | 225 | 230 | 235 | 240 |
| Arg | Pro | Gly | Met | Val | Ser | Thr | Phe | Glu | Gln | Tyr | Gln | Phe | Leu | Tyr | Asp | 245 | 250 | 255 | |
| Val | Ile | Ala | Ser | | | | | | | | | | | | | 260 | | | |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn
1      5      10      15
Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val
20      25      30
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala
35      40      45
Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile
50      55      60
Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu
65      70      75      80
Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val
85      90      95
Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu
100     105     110
Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys
115     120     125
Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly
130     135     140
Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln
145     150     155     160
Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser
165     170     175
Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu
180     185     190
Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys
195     200     205
Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr
210     215     220
Glu Phe Cys Tyr Lys Val Val Gln Glu
225     230

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser
 1 5 10 15
 Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn
 20 25 30
 Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
 35 40 45
 Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp
 50 55 60
 Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met
 65 70 75 80
 Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn
 85 90 95
 Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu
 100 105 110
 Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr
 115 120 125
 Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp
 130 135 140
 Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val
 145 150 155 160
 Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp
 165 170 175
 Glu His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu
 180 185 190
 Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala
 195 200 205
 Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln
 210 215 220
 Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala
 1 5 10 15
 Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile
 20 25 30
 Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Arg Ser Asn Glu Phe Ile Ile
 35 40 45

Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile
50 55 60

Trp Asp His Asn Ala Gln Ile Ile Val Met Leu Pro Asp Asn Gln Ser
65 70 75 80

Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met
85 90 95

Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys
100 105 110

Leu Ser Asn Glu Glu Gln Ile Ile Ile His Asp Phe Ile Leu Glu Ala
115 120 125

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
130 135 140

Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn
145 150 155 160

Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His
165 170 175

Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr
180 185 190

Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val
195 200 205

Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu
210 215 220

Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: /label= Xaa
/note= "For the Consensus Sequence, Xaa = Lack of
Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn
1 5 10 15

Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Gly Thr
35 40 45

Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu
50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp
 65 70 75 80
 Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa
 85 90 95
 Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Xaa Gln Tyr Trp Pro Ser Xaa
 100 105 110
 Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa
 115 120 125
 Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys
 130 135 140
 Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala
 145 150 155 160
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
 165 170 175
 Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser
 180 185 190
 Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala
 195 200 205
 Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa
 210 215 220
 Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu
 225 230 235 240
 Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met
 245 250 255
 Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Xaa Ile Glu Gln Tyr Gln
 260 265 270
 Phe Leu Tyr Lys Val Ile Leu Ser
 275 280